

JUL 08 2003

TECH CENTER 1600/2900



1600

ENTERED

RAW SEQUENCE LISTING

DATE: 07/01/2003

PATENT APPLICATION: US/09/724,666

TIME: 07:54:42

Input Set : N:\Crf3\RULE60\09724666.raw.txt

Output Set: N:\CRF4\07012003\I724666.raw

1 <110> APPLICANT: Sakowicz, Roman
2 Goldstein, Lawrence S. B.
3 The Regents of the University of California
4 <120> TITLE OF INVENTION: Identification and Expression of a Novel Kinesin Motor
5 Protein
6 <130> FILE REFERENCE: 18557C-000710US
7 <140> CURRENT APPLICATION NUMBER: US/09/724,666
8 <141> CURRENT FILING DATE: 2000-11-28
9 <150> PRIOR APPLICATION NUMBER: US/09/235,416A
10 <151> PRIOR FILING DATE: 1999-01-22
11 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US99/01355
W--> 12 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-22
13 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/072,361
W--> 14 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-23
15 <160> NUMBER OF SEQ ID NOS: 7
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 784
20 <212> TYPE: PRT
21 <213> ORGANISM: Thermomyces lanuginosus
22 <220> FEATURE:
23 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed
24 microtubule motor protein
25 <220> FEATURE:
26 <221> NAME/KEY: DOMAIN
27 <222> LOCATION: (1)..(357)
28 <223> OTHER INFORMATION: kinesin-like microtubule motor domain
29 <220> FEATURE:
30 <221> NAME/KEY: DOMAIN
31 <222> LOCATION: (358)..(442)
32 <223> OTHER INFORMATION: neck domain links motor domain to stalk domain
33 <220> FEATURE:
34 <221> NAME/KEY: DOMAIN
35 <222> LOCATION: (443)..(601)
36 <223> OTHER INFORMATION: stalk domain, unc-104 family domain
37 <220> FEATURE:
38 <221> NAME/KEY: DOMAIN
39 <222> LOCATION: (602)..(784)
40 <223> OTHER INFORMATION: tail domain
41 <400> SEQUENCE: 1
42 Met Ser Gly Gly Gly Asn Ile Lys Val Val Val Arg Val Arg Pro Phe
43 1 5 10 15
44 Asn Ala Arg Glu Ile Asp Arg Gly Ala Lys Cys Ile Val Arg Met Glu

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45		20		25		30											
46	Gly	Asn	Gln	Thr	Ile	Leu	Thr	Pro	Pro	Pro	Gly	Ala	Glu	Glu	Lys	Ala	
47			35					40					45				
48	Arg	Lys	Ser	Gly	Lys	Thr	Ile	Met	Asp	Gly	Pro	Lys	Ala	Phe	Ala	Phe	
49			50				55					60					
50	Asp	Arg	Ser	Tyr	Trp	Ser	Phe	Asp	Lys	Asn	Ala	Pro	Asn	Tyr	Ala	Arg	
51		65				70				75					80		
52	Gln	Glu	Asp	Leu	Phe	Gln	Asp	Leu	Gly	Val	Pro	Leu	Leu	Asp	Asn	Ala	
53					85				90						95		
54	Phe	Lys	Gly	Tyr	Asn	Asn	Cys	Ile	Phe	Ala	Tyr	Gly	Gln	Thr	Gly	Ser	
55				100					105				110				
56	Gly	Lys	Ser	Tyr	Ser	Met	Met	Gly	Tyr	Gly	Lys	Glu	His	Gly	Val	Ile	
57			115					120					125				
58	Pro	Arg	Ile	Cys	Gln	Asp	Met	Phe	Arg	Arg	Ile	Asn	Glu	Leu	Gln	Lys	
59		130					135					140					
60	Asp	Lys	Asn	Leu	Thr	Cys	Thr	Val	Glu	Val	Ser	Tyr	Leu	Glu	Ile	Tyr	
61		145				150				155					160		
62	Asn	Glu	Arg	Val	Arg	Asp	Leu	Leu	Asn	Pro	Ser	Thr	Lys	Gly	Asn	Leu	
63				165					170						175		
64	Lys	Val	Arg	Glu	His	Pro	Ser	Thr	Gly	Pro	Tyr	Val	Glu	Asp	Leu	Ala	
65			180						185				190				
66	Lys	Leu	Val	Val	Arg	Ser	Phe	Gln	Glu	Ile	Glu	Asn	Leu	Met	Asp	Glu	
67		195						200				205					
68	Gly	Asn	Lys	Ala	Arg	Thr	Val	Ala	Ala	Thr	Asn	Met	Asn	Glu	Thr	Ser	
69		210				215					220						
70	Ser	Arg	Ser	His	Ala	Val	Phe	Thr	Leu	Thr	Leu	Thr	Gln	Lys	Trp	His	
71		225				230				235					240		
72	Asp	Glu	Glu	Thr	Lys	Met	Asp	Thr	Glu	Lys	Val	Ala	Lys	Ile	Ser	Leu	
73				245					250						255		
74	Val	Asp	Leu	Ala	Gly	Ser	Glu	Arg	Ala	Thr	Ser	Thr	Gly	Ala	Thr	Gly	
75			260					265					270				
76	Ala	Arg	Leu	Lys	Glu	Gly	Ala	Glu	Ile	Asn	Arg	Ser	Leu	Ser	Thr	Leu	
77		275					280					285					
78	Gly	Arg	Val	Ile	Ala	Ala	Leu	Ala	Asp	Met	Ser	Ser	Gly	Lys	Gln	Lys	
79		290				295				300							
80	Lys	Asn	Gln	Leu	Val	Pro	Tyr	Arg	Asp	Ser	Val	Leu	Thr	Trp	Leu	Leu	
81		305			310					315					320		
82	Lys	Asp	Ser	Leu	Gly	Gly	Asn	Ser	Met	Thr	Ala	Met	Ile	Ala	Ala	Ile	
83				325					330					335			
84	Ser	Pro	Ala	Asp	Ile	Asn	Phe	Glu	Glu	Thr	Leu	Ser	Thr	Leu	Arg	Tyr	
85			340					345					350				
86	Ala	Asp	Ser	Ala	Lys	Arg	Ile	Lys	Asn	His	Ala	Val	Val	Asn	Glu	Asp	
87		355					360					365					
88	Pro	Asn	Ala	Arg	Met	Ile	Arg	Glu	Leu	Lys	Glu	Glu	Leu	Ala	Gln	Leu	
89		370				375					380						
90	Arg	Ser	Lys	Leu	Gln	Ser	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Gly	Gly	
91		385			390					395					400		
92	Ser	Gly	Gly	Pro	Val	Glu	Glu	Ser	Tyr	Pro	Pro	Asp	Thr	Pro	Leu	Glu	
93				405					410					415			

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Input Set : N:\Crf3\RULE60\09724666.raw.txt

Output Set: N:\CRF4\07012003\I724666.raw

```

94      Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
95              420                      425                      430
96      Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
97              435                      440                      445
98      Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
99              450                      455                      460
100     Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Leu Gly Ile Ser Ile
101     465              470                      475                      480
102     Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
103              485                      490                      495
104     Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
105              500                      505                      510
106     Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
107              515                      520                      525
108     Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
109     530              535                      540
110     Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
111     545              550                      555                      560
112     Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
113              565                      570                      575
114     Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
115              580                      585                      590
116     His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg
117              595                      600                      605
118     His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His
119     610              615                      620
120     Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg
121     625              630                      635                      640
122     Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
123              645                      650                      655
124     Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
125              660                      665                      670
126     Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
127     675              680                      685
128     Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
129     690              695                      700
130     Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn
131     705              710                      715                      720
132     Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
133              725                      730                      735
134     Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
135              740                      745                      750
136     Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln
137     755              760                      765
138     Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe
139     770              775                      780
141 <210> SEQ ID NO: 2
142 <211> LENGTH: 2352
143 <212> TYPE: DNA

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Output Set: N:\CRF4\07012003\I724666.raw

```

144 <213> ORGANISM: Thermomyces lanuginosus
145 <220> FEATURE:
146 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed
147     microtubule motor protein
148 <400> SEQUENCE: 2
149     atgtcggggtg gtggaaatat caaggtgggtg gtgcgggttac gcccggttcaa cgcccagagaa 60
150     atcgaccgtg gcgcaaaatg tattgtgcgg atggaaggaa atcaaaccat cctcaccct 120
151     cctccgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaag 180
152     gcatttgcgt tcgatcggtc gtattgggtcc ttgacaaga atgctcccaa ctatgcgaga 240
153     caggaagacc tattccaaga tctcggagtc ccgcttctgg ataatgcatt caagggttat 300
154     aacaattgta tcttcgccta cggtcagacc gggtcgggca agtcctattc aatgatgggc 360
155     tatggcaagg agcatggcgt gatcccgcg atttgccagg acatgttccg gcgtattaat 420
156     gaactgcaga aggacaagaa cctcacttgc accgtcgaag ttctgtactt ggaaatttac 480
157     aatgaacgag tgcgagactt gctgaatccg tcgacaaagg ggaatctcaa ggtccgagaa 540
158     cacccgtcga ccggccccta cgtggaggac ttggcgaagc tggtcgtgcy atcattccaa 600
159     gaaatcgaaa atctcatgga tgagggaac aaagccagaa cggttgccgc cacaacatg 660
160     aacgagacat ccagtcgac cccgcgcgtc ttactttga ccttgacgca aaagtggcat 720
161     gatgaagaga ccaaaatgga cacagagaag gttgcgaaga tcagtctggt agatttggcg 780
162     ggttctgagc gagcaacgtc caccggagct actggagcgc gactgaagga gggtcgagag 840
163     atcaaccgct cactttcgac cctaggtcgt gtgattgcag cgctagcgga tatgtcgtcg 900
164     ggaaaacaga agaagaatca gttagtacct taccgagatt cggtaactgac gtggcttctg 960
165     aaggactcct tgggaggcaa ctcgatgacc gccatgattg ccgccatttc gcctgctgat 1020
166     attaactttg aagagactct cagtaccctt cgatatgcgg actctgcgaa gcgaatcaag 1080
167     aaccacgcag tgggtcaatga agaccggaac gcgcggatga tccgcgagtt gaaggaggaa 1140
168     ctgcgcgagc tgaggagcaa actccagagc agtgggtggag gtggaggtgg tgcaggaggt 1200
169     tctggcgggc cagtggagga atcgtaccgc cccgacacgc cgctcgagaa gcaaatcgtg 1260
170     tcgattcagc agccggatgc gacagtcagg aaaatgagca aggcagaaat cgtggagcaa 1320
171     ctgaaccaga gtgagaagct ctatcgggat ctcaatcaga cctgggaaga gaagctggcc 1380
172     aagaccgagg aaatccacaa ggaacgagaa gcggcgctcg aggagctggg tatcagcatc 1440
173     gaaaagggct ttgttggccc ttaccactcc aaagaaatgc cacatctagt caacttgagc 1500
174     gatgacctc ttctggctga gtgtcttgtc tacaacatca agcccgggca gacaagggtt 1560
175     ggaaacgtca accaagatac acaagcggaa attcgtctga acggttcgaa gatcctgaaa 1620
176     gaacactgta cgtttgaaaa tgtggacaac gttgtgacca tcgtgccaaa cgagaaggct 1680
177     gctgtcatgg tgaacggcgt gcgaatcgac aagcctactc gcctccgcag cggctacagg 1740
178     atcatcctgg gcgatttcca catttttoga ttcaaccatc cggaagaagc tcgtgcggaa 1800
179     cggcaagaac aatccttgct tcgccattct gtcaccaaca gtcagttggg ttgcctgct 1860
180     ccaggccgtc acgaccggac actgagcaag gcgggttcgg atgcggacgg cgattctcgc 1920
181     tcagattctc ctttgccgca ctttcgtgga aaggatagcg actggttcta tgctcgagg 1980
182     gaagctgcta gcgcgatcct agggttggat cagaagatct ctcatctgac agatgacgag 2040
183     ttggatgcat tatttgacga tgttcagaaa gcgcgggagc ttctgctgtg gctggtcgaa 2100
184     gacaacgaag atagcgattc gcagagttcg tttccggtcc gtgacaaata catgtccaat 2160
185     ggaaccattg ataatttctc gctcgatacc gccattacta tgccgggtac ccctcgtagt 2220
186     gatgacgacg gtgacgcgct gttttttggt gataagaagt cgaaacagga tgcgtctaata 2280
187     gttgatgttg aggagttgcy tcaacagcag gctcagatgg aagaagccct gaaaacagcg 2340
188     aagcaggaat tc 2352
190 <210> SEQ ID NO: 3
191 <211> LENGTH: 21
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence

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194 <220> FEATURE:
195 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
196 <400> SEQUENCE: 3
197     atgtcgggcg gtggaatat c                                21
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 23
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
205 <400> SEQUENCE: 4
206     gaattcctgc ttogctgttt tca                                23
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 30
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
214     forward primer
215 <220> FEATURE:
216 <221> NAME/KEY: modified_base
217 <222> LOCATION: (25)
218 <223> OTHER INFORMATION: n = a, c, g or t
219 <400> SEQUENCE: 5
W--> 220     gcgcggatcc atytttygcht ayggncarac                    30
222 <210> SEQ ID NO: 6
223 <211> LENGTH: 30
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
228     reverse primer
229 <220> FEATURE:
230 <221> NAME/KEY: modified_base
231 <222> LOCATION: (16)
232 <223> OTHER INFORMATION: n = a, c, g or t
233 <220> FEATURE:
234 <221> NAME/KEY: modified_base
235 <222> LOCATION: (28)
236 <223> OTHER INFORMATION: n = a, c, g or t
237 <400> SEQUENCE: 6
W--> 238     gcgcgaattc tcdganccdg cvarrtcnac                    30
240 <210> SEQ ID NO: 7
241 <211> LENGTH: 30
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
246     reverse primer

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/724,666

DATE: 07/01/2003
TIME: 07:54:43

Input Set : N:\Crf3\RULE60\09724666.raw.txt
Output Set: N:\CRF4\07012003\I724666.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 25
Seq#:6; N Pos. 16,28
Seq#:7; N Pos. 16,28

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09724666.raw.txt

Output Set: N:\CRF4\07012003\I724666.raw

L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD

L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD

L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0

L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0